

Figure 1A
CTGF-4

1 CGGACTTTACCCAGCTCCACTGGAGGACACCTCCTCAGCCCCCAATTCTGCAAGTGGC 60
1 D F T P A P L E D T S S R P Q F C K W P 20

61 CATGTGAGTGCCCGCCATCCCCACCCGCTGCCCGTGGGGGTGAGCCTCATCACAGATG 120
21 C E C P P S P P R C P L G V S L I T D G 40

121 GCTGTGAGTGCTGTAAGATGTGCGCTCAGCAGCTTGGGGACAACGACGAGGCTGCCA 180
41 C E C C K M C A Q Q L G D N C T E A A I 60

181 TCTGTGACCCACCGGGGCTCTACTGTGACTACAGCGGGACCGCCGAGGTACGCAA 240
61 C D P H R G L Y C D Y S G D R P R Y A I 80

241 TAGGAGTGTGTGCACAGGTGGTTCGGTGTGGGCTGCGTCCTGGATGGGGTGCCTACAACA 300
81 G V C A Q V V G V G C V L D G V R Y N N 100

301 ACGGCCAGTCTCTCCAGCCTAAGTGAAGTACAACGACGTCATCGAGGCGCGGTGG 360
101 G Q S F Q P N C K Y N C T C I D G A V G 120

361 GCTGCACACCACTGTGCCTCCGAGTGCGCCCGCGCTCTCTGGTGCCTCCACCGCGGC 420
121 C T P L C L R V R P P R L W C P H P R R 140

421 GCGTGAGCATACCTGGCCACTGCTGTGAGCAGTGGGTATGTGAGGACGACCCAAGAGGC 480
141 V S I P G H C C E Q W V C E D D A K R P 160

481 CACGCAAGACCGCACCCCGTGACACAGGAGCCTTCGATGCTGTGGGTGAGGTGGAGGCAT 540
161 R K T A P R D T G A F D A V G E V E A W 180

541 GGCACAGGAAGTGCATAGCCTACACAAGCCCTGGAGCCCTTGCTCCACAGCTGCGGCC 600
181 H R N C I A Y T S P W S P C S T S C G L 200

601 TGGGGTCTCCACTCGGATCTCCAATGTTAAGCCGAGTGTGGCCTGAGCAAGAGAGCC 660
201 G V S T R I S N V N A Q C W P E Q E S R 220

661 GCCTCTGCAACTTGGCGCCATGCGATGTGGACATCCATACACTCATTAAGGCAGGAAGA 720
221 L C N L R P C D V D I H T L I K A G K K 240

721 AGTGTCTGGCTGTGTACCAGCCAGAGGCATCCATGAACCTTACACTTGCGGGCTGCATCA 780
241 C L A V Y Q P E A S M N F T L A G C I S 260

781 GCACACGCTCCTATCAACCCAAGTACTGTGGAGTTTGCATGGACAATAGGTGCTGCATCC 840
261 T R S Y Q P K Y C G V C M D N R C C I P 280

841 CCTACAAGTCTAAGACTATCGACGTGTCCTTCCAGTGTCTGATGGGCTTGGCTTCTCCC 900
281 Y K S K T I D V S F Q C P D G L G F S R 300

901 GCCAGGTCTATGGATTAATGCCTGCTTCTGTAACCTGAGCTGTAGGAATCCCAATGACA 960
301 Q V L W I N A C F C N L S C R N P N D I 320

961 TCTTTGCTGACTTGAATCCTACCCTGACTTCTCAGAAATTGCCAAGTAGGCAGGCACAA 1020
321 F A D L E S Y P D F S E I A N * 335

1021 ATCTTGGGTCTTGGGGACTAACCAATGCCTGTGAAGCAGTCAGCCCTTATGGCCAATAA 1080

1081 CTTTTCACCAATGAGCCTTAGTTACCCTGATCTGGACCTTGGCCTCCATTCTGTCTCT 1140

IGF-Binding
Domain

vonWillebrand
Factor Type C
Repeat

Sulfated
Glycoconjugate
Binding Motif

C-Terminal
Dimerization &
Receptor-Binding
Domain

Figure 1B
CTGF-4

1141 AACCATTCAAATGACGCCTGATGGTGCTGCTCAGGCCCATGCTATGAGTTTCTCCTTGA 1200

1201 TATCATTACAGCATCTACTCTAAAGAAAAATGCCTGTCTCTAGCTGTTCTGGACTACACCC 1260

1261 AAGCCTGATCCAGCCTTTCCAAGTCACTAGAAGTCCTGCTGGATCTTGCCTAAATCCCAA 1320

1321 GAAATGGAATCAGGTAGACTTTTAATATCACTAATTTCTTCTTTAGATGCCAAACCACAA 1380

1381 GACTCTTTGGGTCCATTCAGATGAATAGATGGAATTTGGAACAATAGAATAATCTATTAT 1440

1441 TTGGAGCCTGCCAAGAGGTACTGTAATGGGTAATTCTGACGTCAGCGCACCAAACTATC 1500

1501 CTGATTCCAAATATGTATGCACCTCAAGGTCATCAAAACATTTGCCAAGTGAGTTGAATAG 1560

1561 TTGCTTAATTTTGATTTTTAATGGAAAGTTGTATCCATTAACCTGGGCATTGTTGAGGTT 1620

1621 AAGTTTCTCTTCACCCCTACACTGTGAAGGGTACAGATTAGGTTTGTCCCAGTCAGAAAT 1680

1681 AAAATTTGATAAACATTCTGTGATGGGAAAAGCCCCAGTTAATACTCCAGAGACAGG 1740

1741 GAAAGGTCAGCCCATTTCAGAAGGACCAATTGACTCTCACACTGAATCAGCTGCTGACTG 1800

1801 GCAGGGCTTTGGGCAGTTGGCCAGGCTCTTCCCTGAATCTTCTCCCTTGCTCTGCTGGG 1860

1861 GTTCATAGGAATTGGTAAGGCCTCTGGACTGGCCTGTCTGGCCCCTGAGAGTGGTGCCCT 1920

1921 GGAACACTCCTCTACTCTTACAGAGCCTTGAGAGACCCAGCTGCAGACCATGCCAGACCC 1980

1981 ACTGAAATGACCAAGACAGGTTTCAGGTAGGGGTGTGGGTCAAACCAAGAAGTGGGTGCC 2040

2041 TTGGTAGCAGCCTGGGGTGACCTCTAGAGCTGGAGGCTGTGGGACTCCAGGGGCCCCCGT 2100

2101 GTTCAGGACACATCTATTGCAGAGACTCATTTACAGCCTTTCGTTCTGCTGACCAAATG 2160

2161 GCCAGTTTTCTGGTAGGAAGATGGAGGTTTACCAGTTGTTTAGAAACAGAAATAGACTTA 2220

2221 ATAAAGGTTTAAAGCTGAAGAGGTTGAAGCTAAAAGGAAAAGGTTGTGTTAATGAATAT 2280

2281 CAGGCTATTATTTATTGTATTAGGAAAATATAATATTTACTGTTAGAATTCTTTTATTTA 2340

2341 GGGCCTTTTCTGTGCCAGACATTGCTCTCAGTGCTTTGCATGTATTAGCTCACTGAATCT 2400

2401 TCACGACAATGTTGAGAAGTTCCCATTTATTATTCTGTTCTTACAAATGTGAAACGGAAG 2460

2461 CTCATAGAGGTGAGAAAACCAACCAGAGTCACCCAGTTGGTGACTGGGAAAGTTAGGAT 2520

2521 TCAGATCGAAATTGGACTGTCTTTATAACCCATATTTCCCCCTGTTTTTAGAGCTTCCA 2580

2581 AATGTGTCAGAATAGGAAAACATTGCAATAAATGGCTTGATTTTTTAATGTCATTTTTCC 2640

Figure 1C
CTGF-4

2641 CTCTTATAGTCTTTCTAGCTCCTTTTCAAAAGACGAGAATATCTGATTTTCTGATAATTT 2700

2701 AGGTGCTTAAGCATCCAAAATACATGGGACACACAAAAATCCAGGAATCCCCTGTAGCTT 2760

2761 ATTCCCTCTTTCCCATCGGAACCAGCTCTCATCACACATTTAAAAGATGATTCTGTTTAC 2820

2821 CCAATGCTGCATATTGAATGTTGTGTAGTTATTCACAGGGAATTCTGTGCAGTGTGCAGA 2880

2881 GAGATTCTTAAACGGGAAAAGGACTGGGAATACATCCTCCTTACTGTGACCTCCCCAAAA 2940

2941 CCTAGTCCAGTGCAAGGTATACAGTGGTGCTCATTAATACTTGATGAATACAGGAAGCT 3000

3001 GTGCATGTGTTCCCTACTTTTTATTCTGAAGCTCTCTTCTTCCAAAGCTACATGAAAATAGAA 3060

3061 TTTTAAACAGTCAAAATTTTATATTAAGTGTCTTAGCAAAAAGAGACATTTAATATTTCAAA 3120

3121 GAAATGCATATGTATGTATACATATATTTGTGTATGCGTATGCAAGAATTCTTGATATAAA 3180

3181 GAGAATTCACCTCCATGAATGATCTCTTCTGTAAGTCAGTGTGAATCATGTTAGATTTTCT 3240

3241 GAGAGTGAAAACACCTGCCATCTACAAATTACAAGGCTGGATAACAGCTCACTCCATTTG 3300

3301 AAATTCAGTGGAAACCCAAGAGCTAGGTTCTTACTGAATTTGCATCTCAATTTGGGAAAC 3360

3361 TGAACCTAGCTTTCAAAGATCATAGGAAGTCTGGTTGGAGAACTAGGGATTATTCTGGC 3420

3421 AATGGGTGGAGGAAGGTGGTCAGAATAACCCAGTCGCCATTGGTTTGGAGAAACGGAAC 3480

3481 ATCTTATGCAGAGCCCGGAGGGCAAGTCTCAAACCCATGGGTGAAGCCATGGAGAAGGA 3540

3541 AATTGGATCCAATGTAATGAAGCTCTTTCTAAGTCAGAATTTCCCTGCAATGGTGTGGC 3600

3601 CTGATTCAATAAAAATTAAGAATAATAAATATAATGGAAAAAAAAAAAAAAAAAAAAA 3658

Figure 2A

| | 10 | 20 | 30 | |
|-----|---|-----------------------------------|-----------|-------------|
| 1 | - - - - - | - - - - - | - - - - - | HWHGU74P.aa |
| 1 | M R W L L P W T L A A V A V L R V G N I L | A T A L S P T P T | | MuELM1.aa |
| 1 | M T - - - - - | - - - - - A A S M G P - - V R - - | | HuCTGF.aa |
| 1 | M S - - - - - | - - - - - S R I A R A L A L - - - | | HuCyr61.aa |
| 1 | M Q - - - - - | - - - - - S V Q S T S F C L R K Q | | HuNOV.aa |
| | 40 | 50 | 60 | |
| 1 | - - D F T P A P L E D T S S R P - - - | Q F C K W P C - - E C | | HWHGU74P.aa |
| 31 | T M T F T P A P L E E T T T R P - - - | E F C K W P C - - E C | | MuELM1.aa |
| 11 | - - - V A F V V L L A L C S R P A V G | Q N C S G P C - - R C | | HuCTGF.aa |
| 12 | - - - - - V V T L L H L - T R L A L S - T | C P A A C - - H C | | HuCyr61.aa |
| 15 | C L C L T F L - L L H L L G Q V A A T | Q R C P P Q C P G R C | | HuNOV.aa |
| | 70 | 80 | 90 | |
| 24 | P P S P - P R C P L G V S L I T D G C E C C K M C A Q Q L G | | | HWHGU74P.aa |
| 56 | P Q S P - P R C P L G V S L I T D G C E C C K I C A Q Q L G | | | MuELM1.aa |
| 36 | P D E P A P R C P A G V S L V L D G C G C C R V C A K Q L G | | | HuCTGF.aa |
| 33 | P L E - A P K C A P G V G L V R D G C G C C K V C A K Q L N | | | HuCyr61.aa |
| 44 | P A T P - P T C A P G V R A V L D G C S C C L V C A R Q R G | | | HuNOV.aa |
| | 100 | 110 | 120 | |
| 53 | D N C T E A A I C D P H R G L Y C D Y S G D R P R Y A I G V | | | HWHGU74P.aa |
| 85 | D N C T E A A I C D P H R G L Y C D Y S G D R P R Y A I G V | | | MuELM1.aa |
| 66 | E L C T E R D P C D P H K G L F C D F G S P A N R - K I G V | | | HuCTGF.aa |
| 62 | E D C S K T Q P C D H T K G L E C N F G A S S T A - L K G I | | | HuCyr61.aa |
| 73 | E S C S D L E P C D E S S G L Y C D R S A D P S N - Q T G I | | | HuNOV.aa |
| | 130 | 140 | 150 | |
| 83 | C - A Q V V G V G C V L D G V R Y N N G Q S F Q P N C K Y N | | | HWHGU74P.aa |
| 115 | C - A Q V V G V G C V L D G V R Y T N G E S F Q P N C R Y N | | | MuELM1.aa |
| 95 | C T A K - D G A P C I F G G T V Y R S G E S F Q S S C K Y Q | | | HuCTGF.aa |
| 91 | C R A Q S E G R P C E Y N S R I Y Q N G E S F Q P N C K H Q | | | HuCyr61.aa |
| 102 | C T A V - E G D N C V F D G V I Y R S G E K F Q P S C K F Q | | | HuNOV.aa |
| | 160 | 170 | 180 | |
| 112 | C T C I D G A V G C T P L C - L R V R P P R L W C P H P R R | | | HWHGU74P.aa |
| 144 | C T C I D G T V G C T P L C - L S P R P P R L W C R Q P R H | | | MuELM1.aa |
| 124 | C T C L D G A V G C M P L C S M D V R L P S P D C P F P R R | | | HuCTGF.aa |
| 121 | C T C I D G A V G C I P L C P Q E L S L P N L G C P N P R L | | | HuCyr61.aa |
| 131 | C T C R D G Q I G C V P R C Q L D V L L P E P N C P A P R K | | | HuNOV.aa |

Figure 2B

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|-----|---|-----|---|-----|---|-----|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|-------------|-----------|
| | | 190 | | 200 | | 210 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 141 | V | S | I | P | G | H | C | C | E | Q | W | V | C | E | D | D | A | K | R | P | R | - | - | - | - | K | T | A | P | R | HWHGU74P.aa | |
| 173 | V | R | V | P | G | Q | C | C | E | Q | W | V | C | D | D | D | A | R | R | P | R | - | - | - | - | Q | T | A | L | L | MuELM1.aa | |
| 154 | V | K | L | P | G | K | C | C | E | E | W | V | C | D | E | P | - | - | - | - | - | - | - | - | K | D | Q | T | V | V | G | HuCTGF.aa |
| 151 | V | K | V | T | G | Q | C | C | E | E | W | V | C | D | E | D | S | I | K | D | P | M | E | D | Q | D | G | L | L | G | HuCyr61.aa | |
| 161 | V | E | V | P | G | E | C | C | E | K | W | I | C | G | P | D | - | - | - | - | - | - | - | - | E | E | D | S | L | G | G | HuNOV.aa |
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Figure 2C

| | 370 | 380 | 390 | |
|-----|---|-----|-----|-------------|
| 285 | T I D V S F Q C P D G L G F S R Q V L W I N A C F C N L S C | | | HWHGU74P.aa |
| 317 | T I S V D F Q C P E G P G F S R Q V L W I N A C F C N L S C | | | MuELM1.aa |
| 300 | T L P V E F K C P D G E V M K K N M M F I K T C A C H Y N C | | | HuCTGF.aa |
| 330 | T V K M R F R C E D G E T F S K N V M M I Q S C K C N Y N C | | | HuCyr61.aa |
| 308 | T I Q A E F Q C S P G Q I V K K P V M V I G T C T C H T N C | | | HuNOV.aa |
| | 400 | 410 | | |
| 315 | R N P N D I - F A D L E S Y P D F S E I A N | | | HWHGU74P.aa |
| 347 | R N P N D I - F A D L E S Y P D F E E I A N | | | MuELM1.aa |
| 330 | P G D N D I - F - E S L Y Y R K M Y G D M A | | | HuCTGF.aa |
| 360 | P H A N E A A F P F Y R L F N D I H K F R D | | | HuCyr61.aa |
| 338 | P K N N E A - F L Q E L E L K T T R G K M | | | HuNOV.aa |

285 317 300 330 308

Figure 3
CTGF-4 Protein Analysis

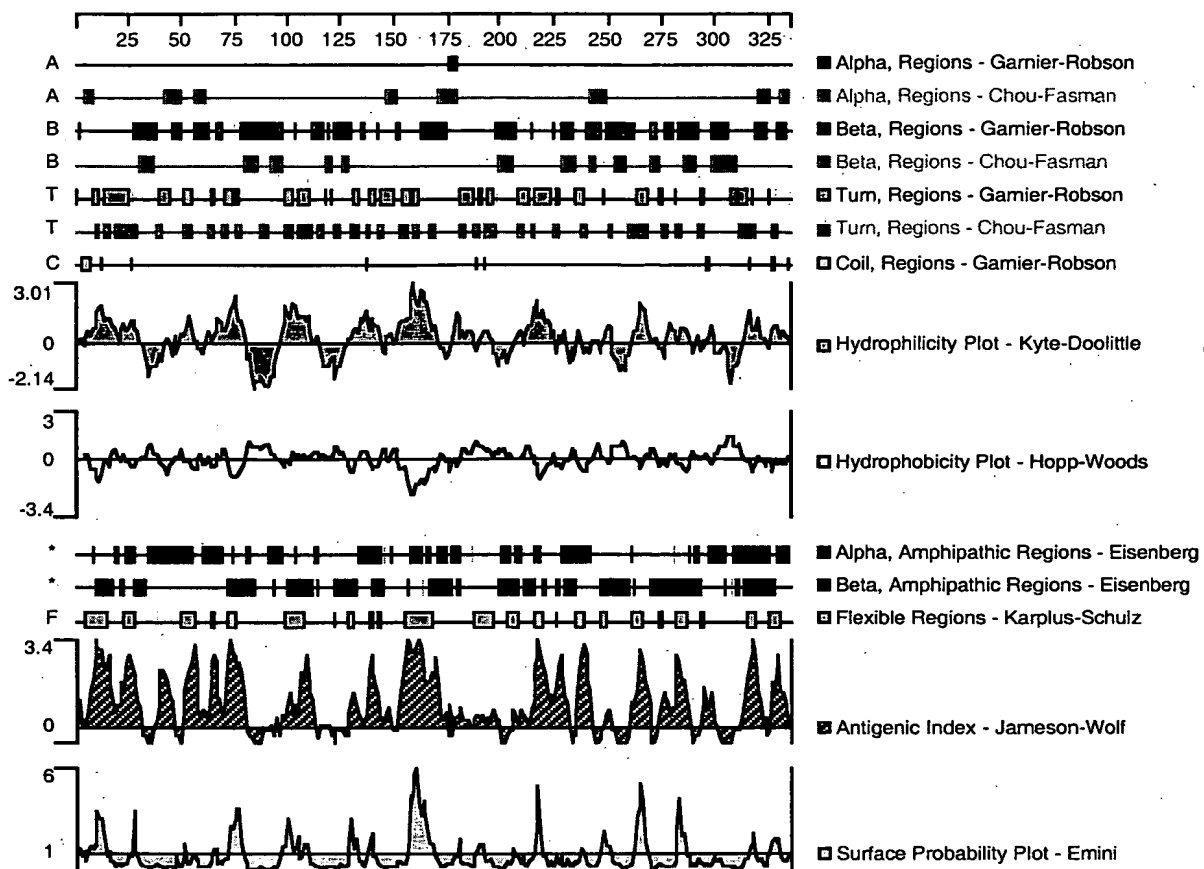


Figure 4

